

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

Wong, M.H.; Oelkers, P.A.
J. Biol. Chem., 270, 272234-272234, 1995
A; Title: Identification of a mutation in the ileal sodium-dependent bile acid transporter
A; Reference number: 138655; PMID: 96070831; PMID: 7552981
A; Accession: I38655
A; Status: Preliminary
A; Molecule type: mRNA
A; Residues: 1-348 <RES>
A; Cross-references: EMBL:010417; NID:9263285; PIDN:AA51870.1; PID:g995399
A; Experimental source: Crohn's disease patient (heterozygous)
A; Note: The wild type is shown; a form with 290-Ser was deficient in transport activity
C; Genetics:
A; Gene: SLC15-A2

Query Match 43.5%; Score 860.5; DB 2; Length 348;
Best Local Similarity 45.6%; Pred. No. 2.2e-63;
Matches 160; Conservative 68; Mismatches 104; Indels 19; Gaps 4;

RESULT 4
155601
Na/taurocholate cotransporting polypeptide - human
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: I155601
B; Hagenbuch, B.; Meier, P.J.
J. Clin. Invest., 92, 1261-1264, 1994
A; Title: Molecular cloning, chromosomal localization, and functional characterization of a gene for Na⁺/taurocholate cotransporting polypeptide in human liver
A; Reference number: 155601; PMID: 9417985; PMID: 8132774
A; Accession: I155601
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-49 <RES>
A; Cross-references: GB:L21893; NID:g410213; PIDN:AAA36381.1; PID:g410214
A; Genetics:
A; Gene: SLC15A2; NTCP
A; Cross-references: GDB:344932; OMIM:182396
A; Map position: 14pter-14qter

Query Match 27.9%; Score 553; DB 2; Length 349;
Best Local Similarity 36.0%; Pred. No. 4.7e-38;
Matches 124; Conservative 77; Mismatches 109; Indels 34; Gaps 10;

Qy 5 CSSSACPANSSEELPVGLEYVGNLLELVFTVSTYMGGLMFSLGCCSVEIRKLMWSHRR 64
Db 14 CSASCACVPESNNNI - - - - - LSVVLSTVLTLLALWMSMGNVEIKFLGHIRR 64

Qy 14 PNSGAVLGLCQFQMPFTAYLLAISFSIKPVQAIAVLMGCGCPGGTISNIFTPEWYDGDMD 124
Db 15 PNSGAVLGLCQFQMPFTAYLLAISFSIKPVQAIAVLMGCGCPGGTISNIFTPEWYDGDMD 124

Qy 125 LSISMTTGSTVAALGMFLCLLTTWASLQLQNLTIPIVQNGITLVCLTIPAFGTYVNY 184
Db 125 LSISMTTGSTVAALGMFLCLLTTWASLQLQNLTIPIVQNGITLVCLTIPAFGTYVNY 184

Qy 185 RWPQSKILKIGAVVCGVLLVAVAGVVLAKGSWNSDITLITISIFPLIGHTVGFL 244
Db 185 RWPQSKILKIGAVVCGVLLVAVAGVVLAKGSWNSDITLITISIFPLIGHTVGFL 244

Qy 245 ALFTHQSKWCRCTISLENGAQN1QMCITMLQLSFTAEHLVQMSFPLAYGLFQOLIDFLI 304
Db 245 ALTAGLPYRCKTVAETGMQNTQLCSTTIVPDTLQVTFPLIYTFQQLAPAAIF 304

Qy 305 VAYQTYKRLKRNKHGRNKGSGTEPVCHTRKSSTSSRETNALEVNEEATTP 355
Db 305 LGFYVAXKK---CHGKOKAEIFE---SKENGTEPESSFYKAN--GGFQP 345

RESULT 3
A41601
Na+/taurocholate transport protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997
C; Accession: A41601
B; Hagenbuch, B.; Foguet, M.; Luebbert, H.; Meier, P.J.
J. Biol. Chem., 267, 18632-18639, 1992
A; Title: Functional expression cloning and characterization of the hepatocyte Na⁽⁺⁾/bile acid transporter
A; Reference number: A41601; PMID: 92073340; PMID: 1661729
A; Accession: A41601
A; Status: Preliminary
A; Molecule type: mRNA
A; Residues: 1-362 <RES>
A; Cross-references: GB:M77429
C; Keywords: transmembrane protein

Query Match 28.3%; Score 559.5; DB 2; Length 362;
Best Local Similarity 37.2%; Pred. No. 1.4e-38;
Matches 133; Conservative 69; Mismatches 125; Indels 21; Gaps 9;

Qy 10 ACAPANSSEELPVGLEYVGNLLELVFTVSTYMGGLMFSLGCCSVEIRKLMWSHRR 69
Db 7 SAPENFS--LPPFGF--FRATDEKALSTLVLMILLIMLGCMEPSKIAHLWKPKGV 62

Qy 70 VGLICQFQMPFTAYLLAISFSIKPVQAIAVLMGCGCPGGTISNIFTPEWYDGDMD 129
Db 63 VALVAQRIMPFLAFLWICKIFHLSNIEALAILIJCSEPGGNUSNLFTAMKGDMNUISVM 122

Qy 130 TTCSTVAALGMPLCIVYT--WSWSLQNLTIPIVQNGITLVCLTIPAFGTYVNYRW 186

RESULT 5
S01696
Gene P3 protein - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 05-Nov-1999
C; Accession: S01696
R; Alcalay, M.; Tonolo, D.
Nucleic Acids Res., 16, 9527-9543, 1988

A;Title: Ctg islands of the X chromosome are gene associated.
 A;Reference number: S01696; MUID:89041548; PMID:3186440

A;Molecule type: DNA
 A;Residues: 1-477 <AIC>

A;Cross-references: EMBL:X12458; PID:g35187; NID:CAA30989.1; PID:g35188

Query Match 16.9%; Score 333.5; DB 2; Length 477;
 Best Local Similarity 31.5%; Pred. No. 7.6e-20;
 Matches 87; Conservative 53; Mismatches 115; Indels 21; Gaps 3;

Qy 1.2 PANSSEBELLPGLEEVHGNELIVETWSTVMGLMFLSGCSVEIRKLWSHIRRPWGIAGV 71

Db 172 PAEDTPATSLADLAHFSENPIYLPLIFUNKCSF -GCCKTELEVKGLMQSPOQMLG 229

Qy 72 LJCQFGAMPETAYLLAISFSKPKVQATAVLMGCCPGETINIFTWVDGMDLSITSMRT 131

Db 230 LUGQFLWMPLYAFLKAKFLPKALAGLITCSPSGGGSYLFSLLGGDVTLAIMTF 289

132 CSTVAALGMMPLCITYLYTWSNQLQNLTIPIQNIGITLVCCLTIPVAFGTUNYRNPQSK 191

Db 290 LSTVAAATGFLPLSSATYRSLLSIHETHLHVPSTS KILGTLFLTAIPAVGLIKSKLPKF SQ 349

Qy 192 IILKIGAVVGVLG-----VVAVGVLVAKGSWSNDITLTISFIPFLIGHVIG 241

Db 350 LLLQQVKPFSVFLLGFLAYRMGYFILAGRL-----PIVLGITVPLVGLVG 400

Qy 242 FULALFTHQSQRCTISLETQAQN1OMCITMLQLS 277

Db 401 YCLATCHKLVPAQRRTVSVIEVQNSLALANLQLS 436

RESULT 6

E69902 probable sodium-dependent transporter yocS - *Bacillus subtilis*

C;Species: *Bacillus subtilis*
 C;Accession: E69902

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodet, P.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hollsappel, S.; Hosono, S.; Hull, M.P.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapridus, A.; Lardinois, A.; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hollsappel, S.; Hosono, S.; Hull, M.P.; Mauel Zegar, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Mauel Zegar, J.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteille, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekimoto, A.; Seron, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshioka, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A;Reference number: A69580; MUID:9804403; PMID:9384377

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
 A;Residues: 1-321 <KIN>

A;Cross-references: GB:Z99114; GB:AU009126; NID:92634230; PID:g2634328

A;Experimental source: strain 168

C;Genetics:

A;Gene: yocS
 C;Superfamily: *Bacillus subtilis* sodium-dependent transporter yocS

Query Match 16.4%; Score 325; DB 2; Length 321;

Best Local Similarity 27.6%; Pred. No. 2.6e-19;
 Matches 84; Conservative 76; Mismatches 114; Indels 30; Gaps 12;

Qy 33 VPTVVSS-TVMGLIMFSLGCSVEIRKLWSHIRRPWGIAGLICLMPFTAYLIA 89

Db 32 LFTWISSYITIPTIGITFCGMGLTQADDKELVKRWQVQVIIQVIAYTIMPVAFCLAFG 91

Qy 90 FSLKPVQAAVLMGCCPGETISNIFTWVDGMDLSISMTCTVAAQNMPLCITYT 149

Db 92 LHLPAEIAVGVLVCCPGGTASNVMTFLAKGNTAISVATTISTLLAPVVTPLUMLFLA 151

Qy 150 WSWSLQQLNTIPYQNGITLV-CLTIPVAFGVVNNYRWPQ-SKII-LKIGAVYGGVLL 205

Db 152 KEW----LPVSPGSLFISIQLQAVFPLTIGLIVMFRRQAVAHALPVSVIG---- 202

Qy 206 LVVAVAGVVLAKGSNN---SDITLTISFIPFLIGHTGFLALLTHQSQRCTISLET 262

Db 203 -IVAVVSAYSGNRNLQSGLLISVVLHNGIGLYLGFLCAKLMKDPSQKIAIEV 261

Qy 263 GAQNQMCITMLQLSFTAELVQMSFLPLA-YGLFOLIDGFLIVAYQTYKRLRNKH-G 320

Db 262 GMQN----SGLGAALATAHSPLAVPSAFLPSVWHNLGSMSL-ATY--WSKRVKKQAG 313

RESULT 7

D90031 hypothetical protein SA2112 [Imported] - *Staphylococcus aureus* (strain N315)

C;Species: *Staphylococcus aureus*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: D90031
 R;Kuroda, M.; Ohta, T.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchima, A.; Mizutani-Uji, Y.; Uchiyama, I.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Oguchi, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:21311152; PMID:11418146

A;Accession: D90031
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:BA000018; PID:g13702121; PID:BA43413.1; GSPPDB:GN00149.

A;Experimental source: strain N315

A;Gene: SA2112
 C;Superfamily: *Bacillus subtilis* sodium-dependent transporter yocS

Query Match 15.2%; Score 301.5; DB 2; Length 305;

Best Local Similarity 27.9%; Pred. No. 2.1e-17;
 Matches 68; Conservative 60; Mismatches 101; Indels 15; Gaps 4;

Qy 41 MMGLIMFSLGCSVERKLWSHIRRPWGIAGLICLMPFTAYLIAISPSLKPQIAV 100

Db 41 LLGIVLGMGTTITIDEKMFVKAHRVIGVQLFSIMTIAFKSPLHPDTAVGV 100

Qy 101 LIMGCCPGGTISNITFWWDGMDLSISMTCTVAAQNMPLCITYTWSLQONLTI 160

Db 101 ILVGCCPGGTSSNVNLYAKANVLSVISITVSTLAPFTPALYFANEWLEYFPLSM 160

Qy 161 PYQNIGITLVCLTIPVAFGV--YNNYRWPQSKILKIGAVYGGVLLUYAVAG--VV 214

Db 161 LWSVQVVL---IPALGIVLQINRKIAEKASTALPISVVAISLIVVGSKHQI 216

Qy 215 LAKGSSWNSDITLTISFIPFLIGHTGFLALLTHQSQRCTISLETGAQNQNCITML 274

Db 217 LTG----LILFLVILHNVLGYTGIVLQARLKDROQKAVSIEVNQNSGIAVSLA 271

Qy 275 QLSF 278

Db 272 ALHF 275

RESULT 8

AD3295 sodium/bile acid cotransporter homolog, sbf family BMF10346 [Imported] - *Brucella melitensis*

C;Species: *Brucella melitensis*
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002

C;Accession: AD3295

RESULTS 9

R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goitsman, E.; Selkov, E.; Blizer, P.H.; Hagiwara, S.; O'Callaghan, D.; Letessier, J.; Mazer, M.; Reference number: AD3252; PMID:11756688

A; Cross-references: GB:AP001510; PIDN:AA51527.1; PID:917982244; GSPDB:GN00190

A; Experimental source: strain 16M

C; Genetics:

A; Gene: BM010346

A; Map position: I

C; Superfamily: *Bacillus subtilis* sodium-dependent transporter yocs

Query Match 15.1%; Score 299.5; DB 2; Length 318;

Best Local Similarity 27.9%; Pred. No. 3.2e-17;

Matches 79; Conservative 66; Mismatches 117; Indels 21; Gaps 7;

RESULTS 10

T02645 hypothetical protein At2g26900 [imported] - *Arabidopsis thaliana*

N; Alternative names: hypothetical protein F12C20.6

C; Species: *Arabidopsis thaliana* (mouse-ear cress)

C; Date: 24-Mar-1999 #text_change 16-Feb-2001

C; Accession: T02645; C84666

R; Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy R; Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy submitted to the EMBL Data Library, August 1998

A; Description: *Arabidopsis thaliana* chromosome II BAC F12C20 genomic sequence.

A; Reference number: Z14685

A; Accession: T02645

A; Molecule type: DNA

A; Residues: 1-338 <ROU>

A; Cross-references: EMBL:AC005168; NID:913426033; PID:3426051

A; Experimental source: cultivar Columbia

R; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R.; Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Fallon, L.; euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-763, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: C84666

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-138 <STO>

A; Cross-references: GB:AB002093; NID:913426051; PIDN:AC32250.1; GSPDB:GN00139

C; Genetics:

A; Gene: AB002093; F12C20.6

A; Map position: 2

A; Introns: 22/2; 61/3; 99/3; 120/3; 163/2; 190/3; 208/1; 240/3; 293/3

Query Match 14.4%; Score 284; DB 2; Length 338;

Best Local Similarity 25.8%; Pred. No. 6.4e-16;

Matches 80; Conservative 54; Mismatches 120; Indels 56; Gaps 8;

RESULTS 11

B83757 sodium-dependent transporter BH0858 [imported] - *Bacillus halodurans* (strain C-125)

C; Species: *Bacillus halodurans*

C; Date: 01-Dec-2000 #text_change 15-Jun-2001

C; Accession: B83757

R; Takami, H.; Nakagawa, K.; Takeki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Y.; Nucleic Acids Res. 28, 4317-4331, 2000

C; Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and reference number: AB3650; PMID:20512582; PMID:11058132

A; Accession: B83757

A; Cross-references: GB:AP001510; PIDN:BA04577.1; GSPDB:GN00125

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-323 <STO>

C; Genetics:

C; Superfamily: *Bacillus subtilis* sodium-dependent transporter yocs

Query Match 15.1%; Score 299.5; DB 2; Length 323;

Best Local Similarity 24.8%; Pred. No. 3.2e-17;

Matches 80; Conservative 80; Mismatches 122; Indels 41; Gaps 9;

RESULTS 12

QY151 SWSLQNLNTIPQNIGITLV-CLTPVAFGVYNNWRPK---QSIIKILKIGAVVGGVLL 206

Db 153 QW---LPI DAKANFVSILOMIITPIALGFVIRMAPNAVDKSPTAVLPHIVSIV AIMAI 206

Qy 207 VVAVAGVVLAKGSWNSDITLTLTISIPLIGHVTCFLLAFLPFTQWQRCTISLETGAQN 266

Db 207 VSAYVGANOANLMSGALLPLAV-MHNFGLLGUYTAKFVGLDESTRAISIVGMON 265

Qy 267 IQMCITMLQISFTAHLVQNLMSPLA-----SPLA-----L-----F-----L----- 325

Db 266 -----SGLGAAAGNHFSPLAALPAIFSVWHNISGPVLVIWS----- 304

Qy 326 CTEVCHTRKSTSRETNAFLEV 348

Db 305 -----RSAKSAQKRQSDADNRKD 322

Qy	270 CITMLQISFT 279		A; Gene: NMB0705 C; Superfamily: <i>Bacillus subtilis</i> sodium-dependent transporter yocS
Db	298 GPILLAQRHFT 307		
		Query Match 13.5%; Score 266.5; DB 2; Length 315; Best Local Similarity 26.6%; Pred. No. 1.e-14; Matches 81; Conservative 65; Mismatches 102; Indels 57; Gaps 10;	
RESULT 11			
F83236	probable transporter PA3264 [imported] - <i>Pseudomonas aeruginosa</i> (strain PA01)		
C; Species: <i>Pseudomonas aeruginosa</i>		Qy	41 MMGLIMFSLGSVEIRKLWSHIRRPGIAVGLLCCFGLMPTAYLIAISFLKPKYQIAV 100
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000		Db	43 LLGIMFMGMGTILKESDFDILFKHKRVAIVGIAFAIMPATAMWLSKLLNPAELAVGV 102
C; Accession: F83236		Qy	101 LIMGCCPGGTISNIFTFWGDMDLSISMTCSTVAALGMPLCITYLYTWSLSQONLT 160
R; Stover, C. K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adam, S.; Yuan, Y.; Brody, L.I.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.		Db	103 ILVGCCPGGTASVNWTYLARGNVVALSVAVTSVSLISPLITP-AIFMLM---AGEMLEI 157
Nature 406: 959-964; 2000		Qy	161 PYQNIGITLV-CLTPVAFGVYVNNRWPQSK-----TILKIGAVVGG---- 201
A; Title: Complete genome sequence of <i>Pseudomonas aeruginosa</i> PA01, an opportunistic pathogen		Db	158 QAGGMLMSIVKMLPVLPIVGLLIVHKVLGSKTEKLTDALPLVSVAIVLIGAVVASKGK 217
Accession number: A82950; MUID:20437337; PMID:10984043		Qy	202 ---GVLLIVVAVAGVYVLAKGWSNSDITLTISFFPLIGHTGFLIALFTHQSQRCT 257
Accession: F83236		Db	218 IMEGLLIFAV---VVLHNG---- 256
A; Molecule type: DNA		Qy	258 ISLETGAQNTOMCITMLQLSFTAELHVOMLSPLA-YGLFOLIDGFLIVAYOTYKRRLK 316
A; Cross-references: GB:AE004749; GB:AE004091; NID:9949388; PIDN:AAG06652.1; GSPDB:GN001		Db	257 LTIEGMQNSGLAAALAAAHAAAAPPV---AVPGALFSWHNNSGSLA---TYWAAKA 309
A; Experimental source: strain PA01		Qy	317 NKHGK 321
C; Genetics: PA3264		Db	310 GRHKK 314
C; Superfamily: <i>Bacillus subtilis</i> sodium-dependent transporter yocS			
RESULT 12			
Qy	32 LVFTVSTVMGILLMFLGSVEIRKLWSHIRRPGIAVGLICQFGIMPFTAYLIAISFS 91		E81937
Db	34 LPITAATAPLLCVMFGMGLTGEDEREVRAHPIRVILGULGAWLLCRLLQ 93		probable transmembrane transport protein NMA0909 [imported] - <i>Neisseria meningitidis</i> (st C; Species: <i>Neisseria meningitidis</i>
Qy	92 LKPVOATAVLYMCCPPTISNIFTFWGDMDLSISMTCSTVAALGMPLCITYLYTWS 151		C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 .
Db	94 LPAEIAVGIVLGVCCPPTASVNMWLSRGDVALSPTTLLAPLVNLASA 153		C; Accession: E81937 R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Qy	152 WSLQQNLTIPYONIGITLV-CLTIPVAFGVYVNNRWPQSKTILKIGAVVGGVLLVAV 210		Holtroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404: 502-506, 2000
Db	154 W---LPVSFAAMFLSILQVVLVPITALGLIAQRQLGERTQVAEVTLPLV-SVFSVII 207		A; Title: Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> Z2491.
Qy	211 AGVVLAKGSNSDITLTISFF----PLIGHTGFLALFTHOSWQRERTISLETGA 264		A; Reference number: A81775; MUID:20222556; PMID:10761919
Db	208 AAVVAASQARTAESGLIMAVMLHNGFLGLLGVTGKLTGMPLAQR----KALAEVGM 263		A; Accession: E81937 A; Status: Preliminary
Qy	265 QNTOMCITMLQLSFTAELHVOMLSPLA-YGLFOLIDGFLIVAYOTYKRRL 315		A; Molecule type: DNA
Db	264 QN----SGLGALANAHFSPIAAVPLAFSWHNNSGSLAALF---RRL 306		A; Cross-references: GB:AU162754; GB:AU157959; NID:97379424; PIDN:CAB84186.1; PMID:9737962
			A; Experimental source: serogroup A, strain Z2491
			C; Genetics:
			C; Superfamily: <i>Bacillus subtilis</i> sodium-dependent transporter yocS
RESULT 13			
B81168	transporter NMB0705 [imported] - <i>Neisseria meningitidis</i> (strain MC58 serogroup B)		Query Match 13.4%; Score 265.5; DB 2; Length 315; Best Local Similarity 25.9%; Pred. No. 2.e-14; Matches 79; Conservative 60; Mismatches 101; Indels 57; Gaps 10;
C; Species: <i>Neisseria meningitidis</i>		Qy	41 MMGLIMFSLGSVEIRKLWSHIRRPGIAVGLLCCFGLMPTAYLIAISFLKPKYQIAV 100
C; Accession: B81168		Db	43 LLGIMFMGMGTILKESDFDILFKHKRVAIVGIAFAIMPATAMWLSKLLNPAELAVGV 102
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Rihi, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.; Science 287: 1809-1815, 2000		Qy	101 LIMGCCPGGTISNIFTFWGDMDLSISMTCSTVAALGMPLCITYLYTWSLSQONLT 160
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve ri, H.; Reference number: A81000; MUID:2017555; PMID:10701307		Db	103 ILVGCCPGGTASVNWTYLARGNVVALSVAVTSVSLISPLITP-AIFMLM---AGEMLEI 157
A; Accession: B81168		Qy	161 PYQNIGITLV-CLTPVAFGVYVNNRWPQSK-----TILKIGAVVGG---- 201
A; Molecule type: DNA		Db	158 QAGGMLMSIVKMLPVLPIVGLLIVHKVLGSKTEKLTDALPLVSVAIVLIGAVVASKGK 217
A; Cross-references: GB:AE002425; GB:AE002098; NID:97225930; PIDN:AAF41122.1; PMID:9722593		Qy	202 ---GVLLIVVAVAGVYVLAKGWSNSDITLTISFFPLIGHTGFLALFTHOSQRCRT 257
A; Experimental source: serogroup B, strain MC58		Db	218 IMEGLLIFAV---VVLHNG---- 256
C; Genetics:			

Qy 258 ISLETGAGNIONCITMLQLSFTAELHVQMLSPPLA-YGLFQOLIDGFLIVAAAYQTYKRRLK 316
 Db 257 LAIEVGMQNSGLAAAALAAHFA---VAFFVAVPGALESFVNINISGSLLA----TYWAAKA 309
 C;Genetics: C;Species: Aquifex aeolicus
 A;Gene: sbt
 C;Superfamily: Bacillus subtilis sodium-dependent transporter yocs
 Query Match 12.6%; Score 250; DB 2; Length 297;
 Best Local Similarity 26.0%; Pred. No. 3.5e-13;
 Matches 81; Conservative 64; Mismatches 126; Indels 40; Gaps 10;

RESULT 14
 DB3438 Probable transporter PA1650 [Imported] - Pseudomonas aeruginosa (strain PAO1)
 C;Species: Pseudomonas aeruginosa
 C;Accession: D83438
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.R.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406: 959-964 2000
 Article: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen reference number: AB2950 ; PMID:20437337 ; PMID:10984043
 Accession: D83438
 Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AB004593; GB:AB004091; NID:9947619; PIDN:AAG05039.1; GSPDB:GN001
 A;Experimental source: strain PA01
 A;Gene: PA1650
 C;Superfamily: Bacillus subtilis sodium-dependent transporter yocs
 Query Match 13.0% ; Score 257.5; DB 2; Length 297;
 Best Local Similarity 26.2%; Pred. No. 8.6e-14;
 Matches 75; Conservative 60; Mismatches 128; Indels 23; Gaps 7;
 Db 33 VFTVVSTTMMGLIMSLGCSVEIRKLWHSIRRPWGIAVGLLQVAVGVLJLVA
 C;Genetics: C;Accession: E070482
 A;Gene: sbt
 C;Species: Aquifex aeolicus
 Query Match 12.6%; Score 250; DB 2; Length 297;
 Best Local Similarity 26.0%; Pred. No. 3.5e-13;
 Matches 81; Conservative 64; Mismatches 126; Indels 40; Gaps 10;

Qy 29 NLELVPTVSVTMMGLI------MFSLGCSVEIRKLWHSIRRPWGI 69
 Db 3 DFSPLILIVSLSLGLPPEFPANIKPLPLPLITIMSLMGLTLPEDFKRIARKRPFIVF 62
 Qy 70 VGLLCQFGLMPTAYLLAISFSLKPVQAIAVLIMGCCPGGTISNLPTFEWVGDMDSLISM 129
 Db 63 YGALLQYVTPMLSGVILSKLFKLPPRLVGVLVGSAPGGTASNLITYLSRGDLSSISM 122
 Qy 130 TTCSCTVAALGMMPCLTYLYTWSLQONLTIPYQNI-GITLVCLTIPVAFGV---YVNY 184
 Db 123 TTTSPLSPLPTVLYLAGKY----VEVPFLSMFETTLKIVTVPLGMVLRFLRY 177
 Qy 185 RWPQKSIKILKIGAVGGVLLVAVGWLAKGSWNSDTULLTISFIPLIGHTTGFLL 244
 Db 178 QINKVEK-FLPFLAVFS-ISLIIVAVIFALNSKLKEFLVLSVLIHNVLGFLIGYL 234
 Qy 245 ALFTHQSWQRCTISLETGAQNTIONCITMLQLSFTAELHVQMLSPPLAYGLFQOLIDGFLI 304
 Db 235 GILAGLDKRYKVALSTEVGHMNSGLS-TVIALKYFS----KVSAIPLSA--IFSLSLON-LI 286
 Qy 305 VAAYQTYKRL 315
 Db 287 GVVLSLIFFRL 297
 Search completed: June 9, 2003, 07:10:12
 Job time : 30 secs

RESULT 15
 ET0482 Na(+) dependent transporter (Sbt family) - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
 C;Accession: E070482
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On
 Nature 392: 353-358 1998
 Article: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
 A;Reference number: A70300; PMID:98196666;
 A;Accession: E070482
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-297 <AQP>
 A;Cross-references: GB:AE000774; PIDN:AAC07854.1; PID:g2984333; GB:AE00065
 A;Experimental source: strain VP5